We claim:

A modified pneumolysin polypeptide having attenuated hemolytic activity wherein said modified pneumolysin polypeptide is obtained by:

- randomly mutating a nucleic acid molecule a) encoding for wild-type pneumolysin to produce mutated nucleic acid molecules encoding modified pneumolysin polypeptides and expressing the mutated nucleic acid molecules in host cells;
- assaying the modilfied polypeptide expressed b) by the host cells\for hemolytic activity;
- identifying the modified pneumolysin c) polypeptides having\substantially similar molecular weight as hative wild-type pneumolysin and which are refoldable.

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A modified properly-refolded pneumolysin polypeptide having attenuated hemolytic activity comprising an amino acid sequ $\!\!\!$ ence of type 14 pneumolysin wherein at least one amino \acid in the region comprising amino acid residues 1 tb 257 is substituted and wherein at least one of said amino acid substitutions results in attenuation of the hemolytic activity of the modified pneumolysin polypeptide.

- The modified pneumolysin polypeptide of claim 2, 25 3. wherein the hemolytic activity is less than 25% compared to wild-type pneumolysin.
  - A modified pneumolysin polypeptide according to claim 4. 3, comprising at least one amino acid substitution in SEQ ID NO.3 the amino acid sequence of Formula Inat residue positions 61, 148, or 195 or the combination of substitutions at residue positions 33, 46, 83, 239 and 257, said Formula 1 comprising

## (Formula I)

	Met 1	Ala	Asn	Lys	Ala 5	Val	Asn	Asp	Phe	Ile 10	Leu	Ala
5	Met	Asn	Tyr 15	Asp	Lys	Lys	Lys	Leu 20	Leu	Thr	His	Gln
	Gly 25	Glu		Ile	Glu	Asn 30	Arg	Phe	Ile	Lys	Glu 35	Gly
10	Asn	Gln	Leu	Pro 40	Asp	Glu	Phe	Val	Val 45	Ile	Glu	Arg
	Lys	Lys 50	Arg	Ser	Leu	Ser	Thr 55	Asn	Thr	Ser	Asp	Ile 60
	Ser	Val	Thr	Ala	Thr 65	Asn	Asp	Ser	Arg	Leu 70	Tyr	Pro
15	Gly	Ala	Leu 75	Leu	Val	Val	Asp	Glu 80	Thr	Leu	Leu	Glu
	85					90		Val			95	
20	Met			100					105			Ser
	Ser	110					115					Asn 120
					125			Asn		130		
25			135					Gln 140				
	145					150					155	His
30				160					165			Asp
		170	_				175					Phe 180
					185			Lys		190		
35			195					200				Val
	Asp 205	Ala	Val	_				Asp			Gln 215	Asp
40	Thr	Val	Thr	Val 220	Glu	Asp	Leu	Lys	Gln 225	Arg	Gly	Ile
	Ser	Ala 230	Glu	Arg	Pro	Leu	Val 235	Tyr	Ile	Ser	Ser	Val 240
	Ala	Tyr	Gly	Arg	Gln 245	Val	Tyr	Leu	Lys	Leu 250	Glu	Thr
45	Thr	Ser	Lys 255	Ser	Asp	Glu	Val	Glu 260	Ala	Ala	Phe	Glu
	Ala 265	Leu	Ile	Lys	Gly	Val 270	Lys	Val	Ala	Pro	Gln 275	Thr

		Glu	Trp	Lys		Ile	Leu	Asp	Asn		Glu	Val	Lys
		Ala	Val	Ile	280 Leu	Gly	Gly		Pro	285 Ser	Ser	Gly	
	_	_	290	** 7	m1	<b>a</b> 1	T	295	7 ~~	Mot	1707	Clu	300
	5	Arg	vaı	vaı	Thr	305	ьуs	vai	Asp	мес	310	Giu	Asp
		Leu	Ile	Gln 315	Glu	Gly	Ser	Arg	Phe 320	Thr	Ala	Asp	His
		Pro	Gly	Leu	Pro	Ile		Tyr	Thr	Thr	Ser		Leu
	10	325					330					335	
		Arg	Asp	Asn	Val 340	Val	Ala	Thr	Phe	Gln 345	Asn	Ser	Thr
		Asp	Tyr	Val	Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn
			350					355					360
	15	Gly	Asp	Leu	Leu	Leu 365	Asp	His	Ser	Gly	Ala 370	Tyr	Val
The State of the S		Ala	Gln	Tyr 375	Tyr	Ile	Thr	Trp	Asn 380	Glu	Leu	Ser	Tyr
	20	Asp 385	His	Gln	Gly	Lys	Glu 390	Val	Leu	Thr	Pro	Lys 395	Ala
Harman Strain	20		Asp	Arg	Asn 400	Gly	Gln	Asp	Leu	Thr 405	Ala	His	Phe
======================================		Thr	Thr	Ser		Pro	Leu	Lys	Gly	Asn	Val	Arg	Asn
Here The Same that the			410					415					420
	25	Leu	Ser	Val	Lys	Ile 425	Arg	Glu	Cys	Thr	Gly 430	Leu	Ala
		Trp	Glu	Trp 435	Trp	Arg	Thr	Val	Tyr 440	Glu	Lys	Thr	Asp
74 55		Leu	Pro	Leu	Val	Arg	Lys	Arg	Thr	Ile	Ser	Ile	Trp
ara:	30	445					450					455	
		Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val		Asp	Lys	Val 0
CL	B	Glu	Asn	Asp	460 ( <b>SE</b>	95	S	٠٥;	3)	465	(-	$\sim$	o Period
	•		470		•								

- The modified pneumolysin according to claim 4, wherein a single amino acid substitution is made and the substituted amino acid is selected from the group consisting of proline or hydroxyproline for position 61; lysine, arginine or histidine for position 148 and leucine, glycine, alanine, isoleucine or valine for position 195.
  - 6. The modified pneumolysin according to claim 3, wherein the substituted amino acids are selected from

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asparagine, glutamine, tyrosine or cycline for positions 33, 46 and 83; lysine, arginine or histidine for position 239 and leucine, glycine, alanine, isoleucine or valine for position 255.

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Modified pneumolysin polypeptide pNVJ1.

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Modified pneumolysin polypeptide pNVJ20/

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Modified pneumolysin polypeptide pNVJ22.

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Modified pneumolysin polypeptide pNVJ45.

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Modified pneumolysin polypeptide pNVJ56.

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Modified pneumolysin polypeptide pNV103.

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Modified pneumolysin polypeptide pNV207 $_{ullet}$ 

Modified pneumolysin polypeptide pNV111.

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Modified pneumolysin polypeptide pNV211.

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A recombinant nucleic acid molecule encoding a modified type 14 pneumolysin polypeptide wherein at least one amino acid in the region comprising amino acid residues 1 to 257 is substituted and wherein at least one of said amino acid substitutions results in attenuation of the hemolytic activity of the modified pneumolysin polypeptide.

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17. The recombinant nucleic acid molecule according to claim 16 comprising the following pneumolysin nucleic acid sequence:

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ATGGCAAATA AAGCAGTAAA TGACTTTATA CTAGCTATGA ATTACGATAA AAAGAAACTC TTGACCCATC AGGGAGAAAG 40

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		{			
	TATTGAAAAT	CGTTTCATCA	AAGAGGGTAA	TCAGCTACCC	120
					160
					200
					240
5					280
3					320
					360
					400
					440
10					480
10					520
					560
					600
					640
15					680
13					720
			TCTCAAGTTG	GAAACCACGA	760
				AAGCTTTGAT	800
		<b>1</b>	CTCAGACAGA	GTGGAAGCAG	840
20		<b>.</b>	GAAGGCGGTT	ATTTTAGGGG	880
_ •		<b>1</b>	CGAGTTGTAA	CAGGCAAGGT	920
	GGATATGGTA	GAGGACTTGA	TTCAAGAAGG	CAGTCGCTTT	960
			GCCGATTTCC	TATACAACTT	1000
	CTTTTTTACG	TGACAATGTA			1040
25	TACAGACTAT	GTTGAGACTA			1080
	GGAGATTTAC				1120
	AATATTATAT	TACTTGGAAT	GAATTATCCT	ATGATCATCA	1160
	AGGTAAGGAA	GTCTTGACTC	The state of the s		1200
	GGGCAGGATT	TAACGGCTCA	1		1240
30			t .		1280
					1320
					1360
	CTATTTGGGG	AACAACTCTC	TATCCGCAGG	TAGAAGATAA	1400
	GGTAGAAAAT	GAC CSECO	ID UO: 1)		1413
			7		
35	and w	herein said	nucleic ac	id sequence compri	ses one
				upstitutions selec	red IIOm
	<b>Δ</b> - 5.0	•G G-54→т\	T-181-C.	$A-196 \rightarrow T$ and $T-302-$	→C;
	11 30	, , , , , , , , ,			
		,	\ <i>Y</i>		
40	A-122	→G. A-514→	G. 1 1583→A	and A-764 $\rightarrow$ G;	
		,		·	
			1		
	A-187	→T, T-380→	A, A-382→C	and $T-443\rightarrow A$ ;	
		,	1		
	T-98-	→C, T-137→C	C, T-248→C,	$T-717\rightarrow A$ and $A-770$	)→G;
		GATGAGTTTG CGACAAATAC CAGTCGCCTC S ACCTTGTTAG GTGCTCCGAT AAGTAGCGAT TCAAGTGTTC GGCATCAAGA 10 AATGCAGTAT CTCAAGGTCA AATCTCTTGA AAAGCAGATT ACAGTCAGCG GTAAGATAC AATTTCTGCA GCTTATGGGC GTAAGAGTCA GCGACCCAAG GGATATGGTA ACAGCAGATC CTTTTTTACG 25 TACAGACTAT GGAGATTTAC AATATTATAT AGGTAAGGAA GGGCAGGATT AGGTAAGGAA GGGCAGGATT 30 TAAAAGGGAA GTGTACCGGG GAAAAAACCG CTATTTGGGG GAAAAAACCG CTATTTGGGG GGAAAAAAT  35 and w Or mo the g A-50-	GATGAGTTTG TTGTTATCGA CGACAAATAC AAGTGATATT CAGTCGCCTC TATCCTGGAG ACCTTGTTAG AGAATAATCC GTGCTCCGAT GACTTATAGT AAGTAGCGAT AGCTTTCTCC TCAAGTGTTC GCGGACCGGT GGCATCAAGA TTATGGTTCAG GGCATCAAGA TTATGATTTT AAAGCAGATT GAAAAAATCA CTCAAGGTCA AGTTTGTTCT ATTCTCTGA TATTGATTTT AAAGCAGATT CAGATTGTTA ACAGTCAGCG TAGACCGTGT ATTCAGAGATAC TGTAACCGTA AATTTCTGCA GAGCGTCCTT GCTTATGGGC GCCAAGTCTA GTAAGAGTGA TGAAGTACAG AAAAGGAGTC AAGGTAGCTC GGAACCAAG TTCGGGTGCC GGATATGGTA GAGGACTTGA ACAGCAGATC ATCCAGGCTT CTTTTTTACG TGACAATGTA ACAGCAGATC TGCCAGGCTCAT GGAGATTAC TGCTGGATCA AATATTATAT TACTTGGAAT AGGTAAGGAA GTCTTGACTC GGGCAGGATT TAACGGCTCA AATATTATAT TACTTGGAAT AGGTAAGGAA TGTTCGTAAT GGGCAGGATT TAACGGCTCA CTATTTGGG AACAACTCTC GGTAGAAAAACCG ATTTGCCACT CTATTTGGGG AACAACTCTC GGTAGAAAAAT GAC SEQ  35  and wherein said or more of the n the group consis A-50→G, G-54→T  40  A-122→G, A-514→  40  A-122→G, A-514→	GATGAGTTTG CGACAAATAC AAGTGATATT CAGTCGCCTC TATCCTGGAG ACCTTGTTAG AGAATAATCC GTGCTCCGAT GACATATAGT AGGTGCTCCGAT GACTTGTTCC GTGCTCCGAT GACTTGTTCC GTGCTCCGAT AGATAATCC GTGCTCCGAT AGCTTTCTCC TCAAGTGTTC GCGCACGGT AAGTGAGAG AACTATATGT AAGTGAGAT AATTCTCTTGA AATCACACACAC CTCAAGGTCA ACTTTGTTC AAAGCAGATT AAAAATCA ACTTTCTTTA AAACCACACAC ATTCTCTTGA AACTTTGTTC AAACCACACAC ATTCTCTTGA ACAGTCACG ATTTTAACAC TTAAAAATCA ACAGTCAGCG TAAAAATCA AATTTTAAGCA AATTTTAACCAT AAATTCTTCAC GCCAAGTTTT AAAAATCCA GCTTAATGGC GCCAAGTTTT GCTTATTGGC GCAAGTTTA GCTTATTGGC GCAAGTTTA GCTTATTGGC GCAAGTTTA AAAATCCA GCAAGTTTA GCTTATTGGC GCAAGTTTA GCTTATTGGC GCAAGTTTA AAAAGCACACACA AAAAGGAGTC ATTTTGGACA AAGGAGTC ATTTTGGACA AAGGAGTC CTCAGACAGA ACCACAGAT CCCAAGTTTC CTCAGACAGA AACGACTAC GCAAGTTTAC GCAAGTACAC GCAAGTTTCC CTCAGACAGA ACCACACAC ATCCAGGCTT CCTCAGACAGA ACCACAGAT ACCAGGATT CCCAGACTAC GCAGATTTAC GCAGATTTAC GCAGATTTAC GCACATAT TCCAGGCTT GCCGATTTCC CTAAGGCTTC CTTTTTTACG GCACAATATCA GCACACACACACACACA ATTCAGACTAT AGGTTACCAG GCAGGATT ACCAGGCTT GCCGATTCC CTAAGGCTTC CTTATCCAGC AATATTATAT AGGTAAGGAA TTCCTGGATCA AGGTTACCAGC TTACCAGC AATATTATAT AGGTAAGGAA TTACCAGCTTA AGGTTACCAGC GCAGGATT TACCGGCTC CTAAGGCTTG CCGATTTCC CTAAGGCTTC CTAAGGCTC AGTTGCCACA AGTTTCCGCAC AATTATCCT CTAAGGCTTC CTAAGGCT CTAAGGCTTC CTAAGGCTTC CTAAGGCTTC CTAAGGCTTC CTAAGGCTTC CTAAGGCT CTAAGGCTTC CTCAGACAC ATTCCAGGC CTATCTGCT CTAAGGCT CTAAGGCT CTAAGGCT CTAAGGCT CTCAGACAC ATTCCAGGC CTATCTC CTCAGACAC ATTCCAGC CTA	GTGCTCCGAT AAGTAGCAT AAGTAGCAT AAGTAGCAT TCAAGTGTTC GCGAACGGT AAACGATTTG TCCAAGCAT TTCAAGTGTTC GCGAACGGT AAACGATTTG TTCAAGTTTC GCGAACGGT AAACGATTTG TTCCCAAGCAT TTATTGTTC GGCATCAAGA TTATTGTTC AATTCTCTTGA AATTCTCTTGA AATTCTCTTGA AATTCTCTTGA AAGTCAAGC AAGTTTGTTC AAACACAGGA AAGTCAAGC AATTCTCTTA AAACACAGCA AAACACAGCA AAACACAGCA TAAAAATCCA GAACATTTTA ACAGTCAGCC TAGACGTGT TAAAAATCCA GAACATTTTA ACAGTCAGCC TAGACGTCTT ACAGTTTA ACAGTCAGCC TAGACGTCTT TTCAAGATTA GCTTATGGC GCCAAGTCTT TTCAAGATTA AACACACGAG GTAAAGCGTC TTTCAAGATTA AACACACGAG GTAAAGCACCA GAACCACCA GTAAAGCACT AACACAACAC

 $T-134\rightarrow C$ ,  $A-305\rightarrow G$ ,  $A-566\rightarrow G$  and  $T-583\rightarrow G$ ;

T-583→G;

T-583→A;

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 $T-443\rightarrow A;$ 

and

10 T-181→C.

18. The recombinant nucleic acid molecule of claim 16 as contained in a vector such as a plasmid, cosmid, bacteriophage or yeast artificial chromosome.

19. A microorganism comprising the nucleic acid molecule of claim 16.

20. The microorganism according to claim 19, wherein the microorganism is selected from the group consisting of bacteria, yeast, mammalian or insect cells.

21. The microorganism according to claim 20, wherein the microorganism is E. coli.

- 22. The modified pneumolysin polypeptide of claim 1, wherein the polypeptide is conjugated to a polysaccharide which elicits antibodies cross-reactive with a bacterial polysaccharide.
- 23. The modified pneumolysin conjugate of claim 22, wherein the polysaccharide is from a bacteria selected from the group consisting of a <u>Haemophilus influenzae</u> type b; meningococcal group A, B or C; group B streptococcus types Ia, Ib, II, III, V or



VNII and pneumococcal.

- 24. A vaccine comprising at least one pneumolysin polypeptide of claim 1 and a pharmaceutically acceptable carrier.
- 25. The vaccine according to claim 24, wherein the polypeptide is conjugated to a polysaccharide which elicits antibodies cross-reactive with a bacterial polysaccharide.
  - 26. The vaccine according to claim 25, wherein the polysaccharide is derived from a bacteria selected from the group consisting of <a href="Haemophilus influenzae">Haemophilus influenzae</a> type b; meningococcus group A, B, or C; group A streptococcus or group B streptococcus serotypes Ia, Ib, II, III, V, or VIII; or one or more of serotypes 1-23 of S. pneumoniae.
  - 27. A method for killing bacteria comprising contacting said bacteria with antibodies to an immunogenic molecule comprising the modified pneumolysin according to claim 1 in the presence of complement.
- 28. The method according to claim 27, wherein the immunogenic molecule is a polysaccharide-polypeptide conjugate wherein the polysaccharide is a bacterial capsular polysaccharide.
  - 29. A method for immunization of mammals comprising administering the vaccine of claim 24 to said , mammals.
  - 30. A method for obtaining modified pneumolysin polypeptides having reduced hemolytic activity and

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being suitable for eliciting an immunogenetic response which is cross-reactive with wild-type pneumolysin comprising the steps of:

- a) randomly mutating a nucleic acid molecule encoding for wild-type pneumolysin to produce mutated nucleic acid molecules encoding modified pneumolysin polypeptides and expressing the mutated nucleic acid molecules in host cells;
- b) assaying the modified polypeptide expressed by the host cells for hemolytic activity;
- c) identifying the modified pneumolysin polypeptides having substantially similar molecular weight as native wild-type pneumolysin and which are refoldable.

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